



Figure S1. RNA Sequencing supporting Data and CellNet classifier validation. (A) Hierarchically clustered heatmap of all significantly differentially expressed genes between sorted and unsorted groups. (B,C) Gene sets within the C5 Gene Ontology (B) and Hallmark (C) GSEA sets with highest and lowest normalized enrichment scores representing sets most highly enriched in sorted and unsorted cells respectively. (D) Validation of training of the CellNet classifier using held-out data from the mouse organogenesis cell atlas fetal days 9.5-13.5. Held-out cells corresponding to each cell type classifier show a generally high classification score, validating the fidelity of the classification algorithm.